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OM nucleic - nucleic search, using sw model

Run on: July 12, 2003, 10:42:21 ; Search time 145 Seconds
(without alignments)
196.013 Million cell updates/sec

Title: US-09-622-964-6

Perfect score: 18

Sequence: 1 caggagagccaccagcc 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1105431 seqs, 789497651 residues

Total number of hits satisfying chosen parameters: 242376

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13.2	73.3	20	9	US-10-156-610-65
2	12.2	67.8	19	9	US-09-982-212-39
3	11.4	63.3	17	10	US-09-866-108-8905
4	11.4	63.3	17	10	US-09-866-108-8906
5	11.4	63.3	17	10	US-09-866-108-8907
6	11.4	63.3	17	10	US-09-866-108-8908
7	11.4	63.3	17	10	US-09-866-108-8909
8	11.4	63.3	20	9	US-09-364-609-3
9	11.2	62.2	16	9	US-09-825-805-18
10	11.2	62.2	17	9	US-09-740-332-63
11	11.2	62.2	17	10	US-09-740-332-4493
12	11.2	62.2	17	10	US-09-866-108-7594
13	11.2	62.2	17	10	US-09-866-108-7595
14	11.2	62.2	19	9	US-10-005-956-860
15	11.2	62.2	20	9	US-10-215-112-9244
16	11.2	62.2	20	9	US-10-215-112-9245
17	11.2	62.2	20	9	US-10-215-112-9248
18	11.2	62.2	20	9	US-10-215-112-9360
19	11.2	62.2	20	9	US-10-215-112-9472

c	20	11.2	62.2	20	9	US-10-215-112-9749	Sequence 9749, Ap
c	21	11.2	62.2	20	9	US-10-215-112-9750	Sequence 9750, Ap
c	22	11.2	62.2	20	9	US-10-215-112-9753	Sequence 9753, Ap
c	23	11.2	62.2	20	9	US-10-215-112-9864	Sequence 9864, Ap
c	24	11.2	62.2	20	9	US-10-215-112-9975	Sequence 9975, Ap
c	25	11.2	62.2	20	9	US-10-016-149-60	Sequence 60, Appl
c	26	11.2	62.2	20	9	US-10-016-149-61	Sequence 61, Appl
c	27	11.2	62.2	20	9	US-09-382-860-269	Sequence 269, App
c	28	10.8	60.0	15	9	US-10-010-802-217	Sequence 217, App
c	29	10.8	60.0	17	9	US-10-060-998-1110	Sequence 1110, Ap
c	30	10.8	60.0	17	9	US-10-060-998-1111	Sequence 1111, Ap
c	31	10.8	60.0	17	9	US-10-060-998-1112	Sequence 1112, Ap
c	32	10.8	60.0	17	9	US-10-060-998-1113	Sequence 1113, Ap
c	33	10.8	60.0	17	10	US-09-759-622-5	Sequence 5, Appl
c	34	10.8	60.0	17	10	US-09-866-108-7592	Sequence 7592, Ap
c	35	10.8	60.0	17	10	US-09-866-108-7593	Sequence 7593, Ap
c	36	10.8	60.0	17	10	US-09-866-108-9829	Sequence 9829, Ap
c	37	10.8	60.0	17	10	US-09-866-108-9830	Sequence 9830, Ap
c	38	10.8	60.0	17	10	US-09-866-108-9831	Sequence 9831, Ap
c	39	10.8	60.0	17	10	US-09-866-108-9832	Sequence 9832, Ap
c	40	10.8	60.0	17	10	US-09-866-108-9833	Sequence 9833, Ap
c	41	10.8	60.0	20	9	US-09-918-026A-58	Sequence 58, Appl
c	42	10.6	58.9	17	9	US-09-827-395A-581	Sequence 581, App
c	43	10.6	58.9	17	9	US-09-740-332-62	Sequence 62, Appl
c	44	10.6	58.9	17	10	US-09-866-108-8929	Sequence 8929, Ap
c	45	10.6	58.9	20	10	US-09-733-294A-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-10-156-610-65
; Sequence 65, Application US/10156610.
; Publication No. US20030050270A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-BETA EXPRESSI
; FILE REFERENCE: ISPH-0666
; CURRENT APPLICATION NUMBER: US/10156,610
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 09/856,246
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: PCT/US99/16959
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: US 09/197,008
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 83
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-156-610-65

Query Match 73.3%; Score 13.2; DB 9; Length 20;
Best Local Similarity 83.3%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGGAGTCGCCACGACC 18
Db 1 CAGGAGTCGCCACGACC 18

RESULT 2
US-09-982-212-39
; Sequence 39, Application US/09982212
; Publication No. US20030118998A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Frank B.

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GAGTCCACCAGC 17
|||||||
Db 4 GAGTCCACCAGC 16

RESULT 5

US-09-866-108-8907
; Sequence 8907, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOmica-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SEQ ID NO 8907
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-8907

Query Match 63.3%; Score 11.4; DB 10; Length 17;
Best Local Similarity 92.3%; Pred. No. 2e+04; Indels 1; Mismatches 0; Gaps 0;
Matches 12; Conservative 0

QY 5 GAGTCCACCAGC 17
|||||||
Db 3 GAGTCCACCAGC 15

RESULT 6

US-09-866-108-8908
; Sequence 8908, Application US/09866108

Query Match 63.3%; Score 11.4; DB 10; Length 17;
Best Local Similarity 92.3%; Pred. No. 2e+04; Indels 1; Mismatches 0; Gaps 0;
Matches 12; Conservative 0

QY 5 GAGTCCACCAGC 17
|||||||
Db 2 GAGTCCACCAGC 14

RESULT 7

US-09-866-108-8909
; Sequence 8909, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

```
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecmica Sequence Listing Engine
; SEQ ID NO 8909
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-8909
```

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Query Match 63.3%; Score 11.4; DB 10; Length 17;
Best Local Similarity 92.3%; Pred. No. 2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GAGTCCCCCAGC 17
DB 1 GAGTCCCCCAGC 13
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RESULT 8
US-09-364-609-3/c
; Sequence 3, Application US/09/364609
; Publication No. US20030036521A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Iliana
; APPLICANT: Brennen, Douglas E.
; APPLICANT: Zamostiano, Rachel
; APPLICANT: Gelber, Edgar
; APPLICANT: Pinhasov, Albert
; APPLICANT: Bassan, Merav
; APPLICANT: Ramot University Authority for Applied Research &
; APPLICANT: Industrial Development, Ltd.
; TITLE OF INVENTION: Methods of Inhibiting Cancer Cells With ADNF III
; FILE REFERENCE: 019856-00010005
; CURRENT APPLICATION NUMBER: US/09/364,609
; CURRENT FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:antisense
US-09-364-609-3
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Query Match 63.3%; Score 11.4; DB 9; Length 20;
Best Local Similarity 92.3%; Pred. No. 2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 3 GGGAGTCCACCA 15
DB 18 GGGAGTCCACCA 6
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```
RESULT 9
US-09-825-805-18/c
; Sequence 18, Application US/09825805
; Publication No. US20030004122A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucle
; FILE REFERENCE: MBH00-831-F (400/009)
; CURRENT APPLICATION NUMBER: US/09/825,805
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/578,223
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 09/476,387
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; NUMBER OF SEQ ID NOS: 1558
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hepatitis C Virus
US-09-825-805-18
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Query Match 62.2%; Score 11.2; DB 9; Length 16;
Best Local Similarity 81.2%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 CAGGGAGTCCACCA 16
DB 16 CAGGCAGTACCACAA 1
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RESULT 10
US-09-740-332-63/c
; Sequence 63, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
```

; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 63
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-63

Query Match 62.2%; Score 11.2; DB 9; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGGGAGTCCACCAG 16
||||| ||| ||||| ||
DB 16 CAGGCAGTACCACAAG 1

RESULT 11
US-09-740-332-4493
; Sequence 4493, Application US/09740332
; Publication No. US2003012570A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4493
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-4493

Query Match 62.2%; Score 11.2; DB 9; Length 17;
Best Local Similarity 75.0%; Pred. No. 2.5e+04;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGGGAGTCCACCAG 16
||||| ||| ||||| ||
DB 1 CAGGCAGUACCACAG 16

RESULT 12
US-09-866-108-7594
; Sequence 7594, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-03-26

; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
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; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 7594
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7594

Query Match 62.2%; Score 11.2; DB 10; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGGGAGTCCACCAGC 17
||||| ||| ||||| ||
DB 2 AGGAAGTCCACCATC 17

RESULT 13
US-09-866-108-7595
; Sequence 7595, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7595
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7595

Query Match 62.2%; Score 11.2; DB 10; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AGGAGTCCACCAGC 17
| | | | | | | | | | | | | | | | |
Db 1 AGGAAGTCCACCAC 16

RESULT 14
US-10-005-956-860
; Sequence 860, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 860
; LENGTH: 19
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-860

Query Match 62.2%; Score 11.2; DB 9; Length 19;
Best Local Similarity 81.2%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAGGAGTCCACCAG 16
| | | | | | | | | | | | | | | | |
Db 3 CAGGATGCCCAACAG 18

RESULT 15
US-10-215-112-9244
; Sequence 9244, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9244
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-9244

Query Match 62.2%; Score 11.2; DB 9; Length 20;
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Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Search completed: July 12, 2003, 11:48:34
Job time : 147 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2003, 09:41:16 ; Search time 1867 Seconds
(without alignments)
280.584 Million cell updates/sec

Title: US-09-622-964-6
Perfect score: 18
Sequence: 1 cagggagtcaccagcc 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 332216

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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20: em_om.*
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41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	11.8	65.6	19	6	AX129446 Sequence
C 3	11.8	65.6	19	6	AX129446 Sequence
C 4	11.4	63.3	17	6	AX132043 Sequence
C 5	11.4	63.3	17	6	AX273032 Sequence
C 6	11.4	63.3	17	6	AX273256 Sequence
C 7	11.4	63.3	17	6	AX273257 Sequence
C 8	11.4	63.3	17	6	AX474915 Sequence
C 9	11.4	63.3	17	6	AX474916 Sequence
C 10	11.4	63.3	17	6	AX474917 Sequence
C 11	11.4	63.3	17	6	AX474918 Sequence
C 12	11.4	63.3	17	6	AX474919 Sequence
C 13	11.4	63.3	19	12	AB068548 Synthetic
C 14	11.4	63.3	20	6	AX055811 Sequence
C 15	11.2	62.2	20	6	AX081461 Sequence
C 16	11.2	62.2	19	6	BD002098 Method an
C 17	11.2	62.2	19	6	BD002141 Method an
C 18	11.2	62.2	20	6	AR167047 Sequence
C 19	11	61.1	20	6	AR210702 Sequence
C 20	11	61.1	17	6	AX474920 Sequence
C 21	10.8	60.0	17	6	AX474921 Sequence
C 22	10.8	60.0	17	6	AR057480 Sequence
C 23	10.8	60.0	17	6	AR057523 Sequence
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C 27	10.8	60.0	17	6	AR115281 Sequence
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C 31	10.8	60.0	18	6	AR169781 Sequence
C 32	10.8	60.0	18	6	AR192805 Sequence
C 33	10.8	60.0	19	6	AR037229 Sequence
C 34	10.8	60.0	19	6	AR048698 Sequence
C 35	10.8	60.0	19	6	AX129445 Sequence
C 36	10.8	60.0	20	6	A04194
C 37	10.8	60.0	20	6	A04223
C 38	10.8	60.0	20	6	AX092588 Sequence
C 39	10.6	58.9	18	6	AR084734 Sequence
C 40	10.6	58.9	18	6	AR105376 Sequence
C 41	10.6	58.9	19	6	AX247498 Sequence
C 42	10.6	58.9	19	6	AX131323 Sequence
C 43	10.6	58.9	19	6	I84487
C 44	10.6	58.9	20	6	A68403 Sequence 8
C 45	10.6	58.9	20	6	AR023735 Sequence

ALIGNMENTS

RESULT 1
AR207367/c
LOCUS AR207367 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 23 from patent US 6372889.
ACCESSION AR207367
VERSION AR207367.1 GI:21506259
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Sheppard,P.O., Conklin,D.C., Farrah,T.M., Maurer,M.F. and Grossmann,A.
TITLE Soluble protein 2TMPO-1
JOURNAL Patent: US 6372889-A 23 16-APR-2002;

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Best Local Similarity 68.9%; Score 12.4; DB 6; Length 20;
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RESULT 2
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AUTHORS
TITLE
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/note="cdk6 ribozyme binding site"
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BASE COUNT
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Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGATCCACACGCC 18
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Db 5 GGATCCACACGCC 19

RESULT 3
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DEFINITION
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||||| |||||
Db 14 GAGTCCACACGCC 1

RESULT 2
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Query Match
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Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 3
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Best Local Similarity 68.9%; Score 12.4; DB 6; Length 20;
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QY 5 GAGTCCACACGCC 18
||||| |||||
Db 14 GAGTCCACACGCC 1

RESULT 2
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DEFINITION
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Best Local Similarity 65.6%; Score 11.8; DB 6; Length 19;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGATCCACACGCC 18
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Db 5 GGATCCACACGCC 19

RESULT 3
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Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 4
AX273032
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
FEATURES
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Location/Qualifiers
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BASE COUNT
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Best Local Similarity 63.3%; Score 11.4; DB 6; Length 17;
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QY 1 CAGGAGTCCAC 13
||||| |||||
Db 2 CAGGAGTCCAC 14

RESULT 5
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DEFINITION
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
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QY 1 CAGGAGTCCAC 13
||||| |||||
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RESULT 5
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LOCUS
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REFERENCE
AUTHORS
TITLE
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BASE COUNT
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Best Local Similarity 63.3%; Score 11.4; DB 6; Length 17;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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||||| |||||

DB 5 CAGGGAGGCCAC 17
 RESULT 6
 AX273257
 LOCUS
 DEFINITION Sequence 826 from Patent WO0162911.
 ACCESSION AX273257
 VERSION AX273257.1 GI:16545994
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS Jarvis,T., von Carlowitz,I., Meswiggen,J.A., Hamblin,P.A. and Ellis,J.H.
 TITLE Method and reagent for the inhibition of grid
 JOURNAL Patent: WO 0162911-A 826 30-AUG-2001;
 FEATURES RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
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 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CAGGGAGTCCAC 13
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 Db 3 CAGGGAGGCCAC 15
 RESULT 7
 AX474915/c
 LOCUS
 DEFINITION Sequence 136 from Patent WO0224750.
 ACCESSION AX474915
 VERSION AX474915.1 GI:22214200
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS Zhang,J.
 TITLE Human kidney tumor overexpressed membrane protein 1
 JOURNAL Patent: WO 0224750-A 136 28-MAR-2002;
 FEATURES Aecomica, Inc. (US)
 source Location/Qualifiers
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 BASE COUNT 3 a 6 c 5 g 3 t
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 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 Db 17 CAGGGAGTCCCTC 5
 RESULT 8
 AX474916/c
 LOCUS
 DEFINITION Sequence 137 from Patent WO0224750.
 ACCESSION AX474916

JOURNAL Patent: WO 0224750-A 139 28-MAR-2002;
Aeomica, Inc. (US)
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BASE COUNT 3 a 4 c 6 g 4 t
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Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAGGGAGTCCAC 13
Db 14 CAGGGAGTCCCTC 2

RESULT 11
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LOCUS AX474919 17 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 140 from Patent WO0224750.
ACCESSION AX474919
VERSION AX474919.1 GI:22214204
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 Zhang, J.
AUTHORS Human kidney tumor overexpressed membrane protein 1
TITLE Patent: WO 0224750-A 140 28-MAR-2002;
JOURNAL Aeomica, Inc. (US)
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BASE COUNT 2 a 4 c 6 g 5 t
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Best Local Similarity 92.3%; Pred. No. 7.9e+05;
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Db 13 CAGGGAGTCCCTC 1

RESULT 12
AB068548/c
LOCUS AB068548 19 bp DNA linear SYN 08-AUG-2001
DEFINITION Synthetic construct DNA, forward primer for human STS sts-D1S2169 at 1p36.
ACCESSION AB068548
VERSION AB068548.1 GI:15129352
KEYWORDS synthetic construct DNA.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Chen, Y.Z., Hayashi, Y., Wu, J.G., Takaoka, E., Maekawa, K., Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H., Morohashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A. and Soeda, E.
TITLE A BAC-based STS-content map spanning a 35-Mb region of human chromosome 1p35-p36
JOURNAL Genomics 74 (1), 55-70 (2001)
MEDLINE 21269192
REFERENCE 2 (bases 1 to 19)
AUTHORS Horii, A.
TITLE Direct Submission

JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai, Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp, Tel: 81-22-717-8042, Fax: 81-22-717-8047)
FEATURES Location/Qualifiers
source 1..19
/organism="synthetic construct"
/db_xref="taxon:32630"
misc_feature 1..19
/note="forward primer for human STS sts-D1S2169 at 1p36 sts-D1S2169 obtained from clones B300M5, B92M14, B97J10, B33P22, B69N18, B179D7, Human BAC library RPC1-11"
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Query Match 63.3%; Score 11.4; DB 12; Length 19;
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Qy 5 GAGTCCACACG 17
Db 17 GAGTCCACACG 5

RESULT 13
AX055811
LOCUS AX055811 20 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 8 from Patent WO0072885.
ACCESSION AX055811
VERSION AX055811.1 GI:12228924
KEYWORDS synthetic construct.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ferber, S.
TITLE Methods of inducing regulated pancreatic hormone production in non-pancreatic islet tissues
JOURNAL Patent: WO 0072885-A 8 07-DEC-2000;
Ferber, Sarah (IL)
FEATURES Location/Qualifiers
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/note="chemically synthesized"
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Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAGGGAGTCCAC 13
Db 8 CTGGAGTCCAC 20

RESULT 14
AX081461/c
LOCUS AX081461 20 bp DNA linear PAT 27-FEB-2001
DEFINITION Sequence 3 from Patent WO0109311.
ACCESSION AX081461
VERSION AX081461.1 GI:13170283
KEYWORDS synthetic construct.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Gozes, I., Brennenman, D.E., Zamostiano, R., Gelber, E., Pinhasov, A. and Basan, M.
TITLE Methods of inhibiting cancer cells with adnf il1 antisense oligonucleotides
JOURNAL Patent: WO 0109311-A 3 08-FEB-2001;

RAMOT UNIVERSITY (IL) : THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
(US)

FEATURES
source

Location/Qualifiers
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/db_xref="taxon:32630"

BASE COUNT 3 a 5 c 6 g 6 t

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RESULT 15

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LOCUS

DEFINITION

Method and kit for detection of specific nucleotide sequence.

ACCESSION

BD002098

VERSION

BD002098.1 GI:18628838

KEYWORDS

JP 2000189198-A/19.

SOURCE

synthetic construct.

artificial sequences.

ORGANISM

1 (bases 1 to 19)

REFERENCE

Ehrlich,H.A., Horne,G.T., Saiki,R.K. and Maris,C.B.

TITLE

Method and kit for detection of specific nucleotide sequence

JOURNAL

F Hoffmann LA ROCHE AG

COMMENT

OS Artificial Sequence

PN JP 2000189198-A/19

PD 11-JUL-2000

PF 24-FEB-2000 JP 200052306

PR 13-MAR-1986 US 839331.22-AUG-1986 US 899344 PI

HENRY ANTHONY EHRLICH, GLENN THOMAS HORNE, RANDALL KEIICHI SAIKI, PI

CURRY BANKS MARIS

PC C12Q1/68//C12N15/09,C12N15/00

CC

FH Key

FT source

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FEATURES

source

Location/Qualifiers

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Best Local Similarity 62.2%; Score 11.2; DB 6; Length 19;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGGAGTCCACAG 16

Db 4 CAGGAGTCCACAG 19

Search completed: July 12, 2003, 11:17:36
Job time : 1871 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run On:

July 12, 2003, 09:40:21 ; Search time 226 seconds
(without alignments)
179.363 Million cell updates/sec

Title: US-09-622-964-6

Perfect score: 18

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	20	AAZ21230
C 2	12.4	68.9	20	20	Human CGICE PCR pr
C 3	12.4	68.9	20	20	Human soluble prot
C 4	12.2	67.8	18	24	Human ZTMO-1 sequ
C 5	11.8	65.6	19	21	Human HLA genotypi
C 6	11.8	65.6	19	21	cdk6 ribozyme bind
C 7	11.8	65.6	19	22	Cyclin B1 ribozyme
C 8	11.8	65.6	19	22	cell-cycle depende
C 9	11.6	64.4	20	21	Cyclin B1 ribozyme
					Hepatitis C genome

C 10	11.4	63.3	17	24	ABQ63360	Human KTM1a porti
C 11	11.4	63.3	17	24	ABQ63361	Human KTM1a porti
C 12	11.4	63.3	17	24	ABQ63362	Human KTM1a porti
C 13	11.4	63.3	17	24	ABQ63363	Human KTM1a porti
C 14	11.4	63.3	17	24	ABQ63364	Human KTM1a porti
C 15	11.4	63.3	17	24	ABN08913	Human GDMPL-1 17-m
C 16	11.4	63.3	17	24	ABN08914	Human GDMPL-1 17-m
C 17	11.4	63.3	17	24	ABN08915	Human GDMPL-1 17-m
C 18	11.4	63.3	17	24	ABN08916	Human GDMPL-1 17-m
C 19	11.4	63.3	17	24	ABN08917	Human GDMPL-1 17-m
C 20	11.4	63.3	18	22	AAH47582	Human Her-3 mRNA 1
C 21	11.4	63.3	20	22	AAF34898	Murine insulin II
C 22	11.4	63.3	20	22	AAC82778	Human chromosome 1
C 23	11.4	63.3	20	24	ABL45263	Cytomegalovirus ta
C 24	11.2	62.2	16	14	AAQ52859	Human GDMPL-1 17-m
C 25	11.2	62.2	17	24	ABN07602	Human GDMPL-1 17-m
C 26	11.2	62.2	17	24	ABN07603	Probe DB185, Synt
C 27	11.2	62.2	18	13	AAQ26466	Sequence of probe
C 28	11.2	62.2	19	8	AAAT71284	Allele-specific pr
C 29	11.2	62.2	19	10	AAAN90050	HLA-DQbeta probe G
C 30	11.2	62.2	19	12	AAQ15037	Probe GH61 derived
C 31	11.2	62.2	19	12	AAQ15104	Antisense oligonuc
C 32	11.2	62.2	20	15	AAQ44888	Dog genomic marker
C 33	11.2	62.2	20	21	AAA66799	Human dysferlin ex
C 34	11.2	62.2	20	21	AAA37007	Human TGF-beta1 pr
C 35	11.2	62.2	20	22	AAD13533	Human KTM1a porti
C 36	11.1	61.1	17	24	ABQ63365	Human KTM1a porti
C 37	11.1	61.1	17	24	AAV08217	PCR primer ABCR.EX
C 38	11.1	61.1	18	19	ABQ63366	Rat VRI antisense
C 39	10.8	60.0	14	24	ABL94636	Human IL4Ralpha ge
C 40	10.8	60.0	15	22	AAF69574	Rat VRI antisense
C 41	10.8	60.0	16	24	ABL94637	Rat VRI antisense
C 42	10.8	60.0	17	16	AAAT53533	Rat ICAM hammerhea
C 43	10.8	60.0	17	16	AAAT53518	Rat ICAM hammerhea
C 44	10.8	60.0	17	16	AAAT53448	Rat ICAM hammerhea
C 45	10.8	60.0	17	16	AAAT53757	Rat ICAM hammerhea

ALIGNMENTS

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RESULT 1
AAZ21230
ID  AAZ21230 standard; DNA; 18 BP.
XX
AC  AAZ21230;
XX
DT  22-NOV-1999 (first entry)
XX
DE  Human CGICE PCR primer SEQ ID NO:6.
XX
KW  CGICE; Best's macular dystrophy; mutation; diagnosis; detection;
KW  BMD; age-related macular dystrophy; PCR primer; ss.
XX
OS  Synthetic.
OS  Homo sapiens.
XX
PN  WO9943695-A1.
XX
PD  02-SEP-1999.
XX
PF  22-FEB-1999; 99WO-US03790.
XX
PR  25-FEB-1998; 98US-0075941.
XX  18-DEC-1998; 98US-0112926.
XX
PA  (MERI ) MERCK & CO INC.
XX  (UYUP-) UNIV UPPSALA.
XX
PI  Petrukhin K, Caskey CT, Metzker M, Wadelius C;
XX  WPI; 1999-540560/45.
XX

```

PT Human and mouse polynucleotides encoding GCLCE polypeptides -
PS Disclosure; Page 17; 67pp; English.
XX
CC The present invention describes human and mouse GCLCE polynucleotides
CC and proteins. When the GCLCE gene is mutated it is responsible for
CC Best's macular dystrophy (BMD). Polynucleotides encoding GCLCE are
CC useful for diagnosing whether a patient carries a mutation in the
CC GCLCE gene. Normal and mutated GCLCE proteins are useful for
CC identifying activators and/or inhibitors of these proteins, in order
CC to treat BMD. The GCLCE gene offers a simpler and cheaper method of
CC diagnosing BMD without the need for the presence of the patient. The
CC gene may also be useful for discovering the genetic cause of age-related
CC macular dystrophy. The present sequence represents a PCR primer for
CC the human GCLCE cDNA sequence.
XX
SQ Sequence 18 BP; 4 A; 8 C; 5 G; 1 T; 0 other;
Query Match 100.0%; Score 18; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGGGAGTCCACCGCC 18
Db 1 CAGGGAGTCCACCGCC 18
|||||
RESULT 2
AAZ24791/c
ID AAZ24791 standard; DNA; 20 BP.
XX
AC AAZ24791;
XX
DT 31-JAN-2000 (first entry)
XX
DE Human soluble protein ZTMPO-1 DNA sequencing primer ZC16037.
XX
KW Soluble protein; ZTMPO-1; thymopoietin-emerin family; human; cancer;
KW nuclear membrane protein; cardiac disorder; autoimmune disease; testis;
KW infectious disease; cellular proliferation; skeletal muscle; thyroid;
KW adrenal gland; tumor; spermatogenesis; sperm activation; PCR primer;
KW contraindication; immune response; humoral response; vaccination; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO954468-A1.
XX
PD 28-OCT-1999.
XX
PF 19-APR-1999; 99WO-US08601.
XX
PR 21-APR-1998; 98US-0063838.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Sheppard PO, Conklin DC, Farrah TM, Maurer MF, Grossmann A;
XX WPI; 1999-634003/54.
XX
DR New isolated ZTMPO-1 polypeptides used for diagnosis and treatment of
PT e.g. cancer, cardiac and autoimmune disorders and infectious diseases
PT and for developing contraceptives -
PS Example 1; Page 102; 110pp; English.
XX
CC The invention provides a human soluble protein ZTMPO-1 which has
CC homology to the thymopoietin-emerin family of nuclear membrane proteins.
CC The ZTMPO-1 protein can be expressed by standard recombinant
CC methodology. Altered levels of ZTMPO-1 receptor polypeptides may be
CC indicative of pathological conditions including cancer, cardiac and
CC autoimmune disorders and infectious diseases. The nucleic acid can be
CC used as a source of hybridization probes for detecting a genetic

CC abnormality in a patient. The ZTMPO-1 polypeptides can be used to
CC modulate cellular proliferation and differentiation in a diverse array of
CC tissues such as testis, skeletal muscle, thyroid and adrenal gland.
CC Antagonists of ZTMPO-1 can be used in modulating cellular proliferation
CC and differentiation such as in tumor growth and development. They can
CC also be used for inhibiting spermatogenesis and sperm activation. Such
CC ZTMPO-1 antagonists can be used for contraception in humans and animals,
CC and in particular, domestic and zoological animals and livestock, where
CC they would act to prevent fertilization of an egg. ZTMPO-1 antagonists
CC could also be used to mediate immune response, e.g. by boosting the
CC humoral response in individuals at risk for an infectious disease or as
CC a supplement to vaccination. Sequences AAZ24777-791 represent primers
CC used for sequencing the ZTMPO-1 DNA.
XX
SQ Sequence 20 BP; 4 A; 5 C; 8 G; 3 T; 0 other;
Query Match 68.9%; Score 12.4; DB 20; Length 20;
Best Local Similarity 92.9%; Pred. No. 8.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 GAGTCCACCGCC 18
Db 14 GAGTCCACCGCC 1
|||||
RESULT 3
ABK50010/c
ID ABK50010 standard; DNA; 20 BP.
XX
AC ABK50010;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human ZTMPO-1 sequencing primer ZC16037.
XX
KW ZTMPO; human; immunosuppressive; inotropic; cardiac; leukaemia;
KW cardiant; cytostatic; antidiabetic; hypotensive; immunological; ss;
KW reproductive; muscle pathology; diabetes; muscular dystrophy;
KW haematopoietic disorder; hypertension; chromosome 12q24.33;
XX
OS Homo sapiens.
XX
PN US6372889-B1.
XX
PD 16-APR-2002.
XX
PF 19-APR-1999; 99US-0294531.
XX
PR 21-APR-1998; 98US-082513P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Sheppard PO, Conklin DC, Farrah TM, Maurer MF, Grossmann A;
XX WPI; 2002-350566/38.
XX
DR Novel isolated ZTMPO-1 polypeptide, useful for modulating cell
PT proliferation, and for treating disorders such as diabetes, muscular
PT dystrophy and hypertension -
PS Example 1; Column 63; 40pp; English.
XX
CC This invention relates to the cDNA and protein sequences of a novel
CC isolated ZTMPO-1 polypeptide. ZTMPO-1 is a soluble protein with
CC homology to the nuclear membrane proteins emerlin and thymopoietins.
CC The protein of the invention may have immunosuppressive, inotropic,
CC cardiant, cytostatic, antidiabetic and hypotensive activities. The
CC invention also comprises antibodies to ZTMPO-1 proteins which can
CC be used to detect ZTMPO proteins and may be used to regulate the
CC function of the protein. The sequences of the invention may be used
CC for modulating cellular proliferation and differentiation, and
CC for diagnostic purposes. The polypeptides can be used to treat

CC immunological, reproductive, cardiac, and muscle pathologies, such as
CC diabetes, muscular dystrophy, haematopoietic disorders, leukaemias, and
CC hypertension. The present sequence represents a human ZPMO-1 gene
CC sequencing primer used to sequence the ZPMO gene of the invention.
XX
SQ Sequence 20 BP; 4 A; 5 C; 8 G; 3 T; 0 other;

Query Match 68.9%; Score 12.4; DB 24; Length 20;
Best Local Similarity 92.9%; Pred. No. 8.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GAGTCCACCAGCC 18
|||||||
DB 14 GAGTCCACCAGCC 1

RESULT 4
ABL30611/c
ID ABL30611 standard; DNA; 18 BP.
AC ABL30611;
XX
DT 21-MAR-2002 (first entry)
XX
DE Human HLA genotyping oligonucleotide SEQ ID NO 100.
XX
KW Human; human leukocyte antigen; HLA; genotype; polymorphism;
KW immunogenetic; transplantation; genetic disease; ss.
XX
OS Homo sapiens.
XX
PN WO200192572-A1.
XX
PD 06-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-JP04662.
XX
PR 01-JUN-2000; 2000JP-0164798.
XX
PS (NLSN) NISSHINBO IND INC.
PA (SYST-) SYSTEM RES INC.
XX
PI Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
XX
DR WPI; 2002-122074/16.

Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes
of individuals e.g. by determining immunogenetic differences when
transplanting between them -
Claim 10; Page 112; 345pp; Japanese.
The invention relates to a typing kit for judging human leukocyte antigen
(HLA) genotype of a sample by hybridising a substrate on which 10-24 base
oligonucleotides (ABL30513-ABL31809) originating in the sequences of
genes e.g. belonging to HLA class I antigens on human genome and
containing gene polymorphisms as alloantigens have been immobilised as
primers for amplification of cleaved nucleic acids relating to gene
polymorphisms. The method is useful for judging HLA genotypes of
individuals by determining immunogenetic differences before transplanting
between them, providing genetic information to decide compatibility of
organ and tissue for transplantation e.g. of bone marrow, kidney, liver,
pancreas, Langerhans islet in pancreas and cornea, susceptibility
diagnosis of genetic diseases and identifying individuals.
Sequence 18 BP; 0 A; 6 C; 8 G; 4 T; 0 other;

Query Match 67.8%; Score 12.2; DB 24; Length 18;
Best Local Similarity 82.4%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CAGGAGTCCACCAGC 17
|||||
The present invention relates to a hairpin or hammerhead ribozyme, cleaves
RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PCNA and Cyclin B1 -
Disclosure; Page 56; 109pp; English.
The present invention relates to a hairpin or hammerhead ribozyme,
designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells.
CC The ribozyme is resistant to endonuclease activity and hence is
CC efficient in restenosis treatment.
Sequence 19 BP; 3 A; 9 C; 3 G; 4 T; 0 other;

DB 18 CAGGAGTCCACCAGC 2

RESULT 5
AAA83078
ID AAA83078 standard; DNA; 19 BP.
XX
AC AAA83078;
XX
DT 04-DEC-2000 (first entry)
XX
DE cdk6 ribozyme binding site #138.
XX
KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
KW restenosis; ss.
XX
OS Mammalia.
XX
PN WO200032765-A2.
XX
PD 08-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US28772.
XX
PR 04-DEC-1998; 98US-Q110954.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
DR WPI; 2000-412314/35.

New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PCNA and Cyclin B1 -
Disclosure; Page 56; 109pp; English.
The present invention relates to a hairpin or hammerhead ribozyme,
designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells.
CC The ribozyme is resistant to endonuclease activity and hence is
CC efficient in restenosis treatment.
Sequence 19 BP; 3 A; 9 C; 3 G; 4 T; 0 other;

Query Match 65.6%; Score 11.8; DB 21; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.7e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 GGAGTCCACCAGCC 18
|||||
DB 5 GGATCCACCAGCC 19
|||||

RESULT 6
AAA85675/c
ID AAA85675 standard; DNA; 19 BP.
XX
AC AAA85675;
XX
DT 04-DEC-2000 (first entry)
XX
DE Cyclin B1 ribozyme binding site #4.
XX
KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
KW restenosis; ss.
XX
OS Mammalia.

PN WO200032765-A2.
 XX 08-JUN-2000.
 XX 06-DEC-1999; 99WO-US28772.
 XX 04-DEC-1998; 98US-0110954.
 XX (IMMU-) IMMUSOL INC.
 XX Tritz R, Welch PJ, Barber JR, Robbins JM;
 XX WPI; 2000-412314/35.
 XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 XX RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 XX PCNA and Cyclin B1
 XX Disclosure; Page 96; 109pp; English.
 XX The present invention relates to a hairpin or hammerhead ribozyme,
 XX designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 XX other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 XX Representative examples of ribozyme recognition sites are given in
 XX AAA2415 to AAA86787. The ribozyme of the invention is useful for
 XX inhibiting restenosis by introduction of the ribozyme into cells.
 XX The ribozyme is resistant to endonuclease activity and hence is
 XX efficient in restenosis treatment.
 XX Sequence 19 BP; 0 A; 5 C; 9 G; 5 T; 0 other;
 SQ Query Match 65.6%; Score 11.8; DB 21; Length 19;
 Best Local Similarity 86.7%; Pred. No. 1.7e+04;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 GGAGTCCCGACCGCC 18
 DB 17 GGAGCCCGACCGCC 3
 RESULT 7
 AAH58240
 ID AAH58240 standard; DNA; 19 BP.
 XX AAH58240;
 AC AAH58240;
 DT 10-SEP-2001 (first entry)
 DE Cell-cycle dependent kinase cdk6 ribozyme binding site SEQ ID NO:664.
 XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnary;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytosstatic;
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
 KW atopic dermatitis; actinic keratosis; gene therapy; viral wart;
 KW basal cell carcinoma; seborrheic wart; squamous cell carcinoma;
 KW sickle cell retinopathy; ss.
 XX Homo sapiens.
 OS Synthetic.
 PN WO200130362-A2.
 XX 03-MAY-2001.
 XX 26-OCT-2000; 2000WO-US29500.
 XX 26-OCT-1999; 99US-0161532.
 XX (IMMU-) IMMUSOL INC.
 PA

Robbins JM, Tritz R;
 WPI; 2001-300427/31.
 Treating proliferative skin or eye diseases and scarring, using
 ribozymes that cleave RNA encoding cytokines involved in inflammation,
 matrix metalloproteinases, growth factors and cell-cycle dependent
 kinases -
 Example 1; Page 120; 408pp; English.
 The present invention describes a method for treating a proliferative
 skin or eye disease and scarring. The method involves administering a
 ribozyme (I) which cleaves RNA encoding a cytokine involved in
 inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 dependent kinase, growth factor or a reductase, or administering a
 nucleic acid molecule (II) comprising a promoter operably linked to a
 nucleic acid segment encoding (I). (I) can have antipsoriatic,
 dermatological, cytosstatic, antiseborrheic, antidiabetic, antiskickling,
 ophthalmological, vulnary, keratolytic and virucide activities, and
 cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 in gene therapy. (I) and (II) are useful for treating proliferative
 skin diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 squamous or basal cell carcinoma and viral or seborrheic wart. They can
 also be used for treating proliferative eye diseases such as diabetic
 retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 prematurity and retinal detachment, and for treating and preventing
 scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 scar. AAH57577 to AAH62099 represent sequences used in the
 exemplification of the present invention.
 SQ Sequence 19 BP; 3 A; 9 C; 3 G; 4 T; 0 other;
 Query Match 65.6%; Score 11.8; DB 22; Length 19;
 Best Local Similarity 86.7%; Pred. No. 1.7e+04;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 GGAGTCCCGACCGCC 18
 DB 5 GGATTCCTCCACCTGCC 19
 RESULT 8
 AAH60837/C
 ID AAH60837 standard; DNA; 19 BP.
 XX AAH60837;
 AC AAH60837;
 DT 10-SEP-2001 (first entry)
 DE Cyclin B1 ribozyme binding site SEQ ID NO:3261.
 XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnary;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytosstatic;
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
 KW atopic dermatitis; actinic keratosis; gene therapy; viral wart;
 KW basal cell carcinoma; seborrheic wart; squamous cell carcinoma;
 KW sickle cell retinopathy; ss.
 XX Homo sapiens.
 OS Synthetic.
 PN WO200130362-A2.
 XX 03-MAY-2001.
 XX 26-OCT-2000; 2000WO-US29500.
 XX

PR 26-OCT-1999; 990S-0161532.
 PA (IMMU-) IMMUSOL INC.
 XX Robbins JM, Tritz R;
 PI WPI; 2001-300427/31.
 DR Treating proliferative skin or eye diseases and scarring, using
 XX ribozymes that cleave RNA encoding cytokines involved in inflammation,
 PT kinases -
 PT Example 1; Page 309; 408pp; English.
 XX The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antiproliferative,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
 CC ophthalmological, vulvar, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative
 CC skin diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH5757 to AAH62099 represent sequences used in the
 CC exemplification of the present invention.
 XX Sequence 19 BP; 0 A; 5 C; 9 G; 5 T; 0 other;
 SQ
 Query Match 65.6%; Score 11.8; DB 22; Length 19;
 Best Local Similarity 86.7%; Pred. No. 1.7e+04;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 4 GGAGTCCCGACGACC 18
 DB 17 GGAGCCCGACGACC 3
 RESULT 9
 AA288591
 ID AA288591 standard; DNA; 20 BP.
 AC AA288591;
 DT 04-MAY-2000 (first entry)
 DE Hepatitis C genome PCR primer 4.
 XX Detection; serum; plasma; probe; infection; PCR primer; ss.
 KW Hepatitis C virus.
 XX DB19832050-A1.
 PN 27-JAN-2000.
 XX 16-JUL-1998; 98DE-1032050.
 XX 16-JUL-1998; 98DE-1032050.
 PR (BIOT) BIOTEST PHARMA GMBH.
 PA Jochum C;
 XX WPI; 2000-148478/14.
 PT

XX Detection of Hepatitis C and B viral genomes in serum or plasma using
 PT specific oligonucleotide primers and probes -
 XX Claim 1c; Page 2; 7pp; German.
 PS This invention describes a novel method to detect Hepatitis C (HCV)
 XX and/or Hepatitis B (HBV) viral genomes in a serum or plasma sample using
 CC specific primers and probes. The method and oligonucleotide primers and
 CC probes are useful for the specific detection of Hepatitis C and/or
 CC Hepatitis B viral sequences in plasma and serum samples. This may be
 CC useful for preventing Hepatitis B and/or C infection in patients through
 CC contaminated blood and/or serum products. The method is able to detect
 CC all reference samples of HBV subtypes AD and AY and HCV subtypes 1 - 5
 CC with 100% accuracy. AA288588-288591 represent PCR primers used to detect
 CC HCV virus in a sample.
 XX Sequence 20 BP; 6 A; 7 C; 5 G; 2 T; 0 other;
 SQ
 Query Match 64.4%; Score 11.6; DB 21; Length 20;
 Best Local Similarity 77.8%; Pred. No. 2.1e+04;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 1 CAGGAGTCCCGACGACC 18
 DB 1 CAGGAGTCCCGACGACC 18
 RESULT 10
 ABQ63360/C
 ID ABQ63360 standard; DNA; 17 BP.
 XX AC ABQ63360;
 XX DT 20-AUG-2002 (first entry)
 DE Human KTOM1a portion (ABQ63232) probe # 73.
 XX Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
 KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
 KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
 XX Homo sapiens.
 OS WO200224750-A2.
 PN 28-MAR-2002.
 XX 21-SEP-2001; 2001WO-US29656.
 XX 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 PR 30-JAN-2001; 2001WO-US00661.
 PR 30-JAN-2001; 2001WO-US00662.
 PR 30-JAN-2001; 2001WO-US00663.
 PR 30-JAN-2001; 2001WO-US00664.
 PR 30-JAN-2001; 2001WO-US00665.
 PR 30-JAN-2001; 2001WO-US00666.
 PR 30-JAN-2001; 2001WO-US00667.
 PR 30-JAN-2001; 2001WO-US00668.
 PR 30-JAN-2001; 2001WO-US00669.
 PR 23-MAY-2001; 2001US-0864761.
 PR 28-AUG-2001; 2001US-315676P.
 XX (AEOM-) AEOMICA INC.
 PA Zhang J;
 XX WPI; 2002-479509/51.
 XX New human kidney tumor overexpressed membrane (KTOM1) protein and
 PT

PT nucleic acids encoding the protein, useful for treating subjects having
 PT defects in Ktomi1 which can manifest as cancer of the kidney, or as a
 PT disorder of e.g., liver or bone
 XX
 PS Example 2; Page 167; 418pp; English.
 XX
 CC The invention relates to a novel isolated nucleic acid encoding human
 CC Ktomi1 (kidney tumour overexpressed membrane) protein. The protein of the
 CC invention has cytostatic activity. The nucleotide may have a use in gene
 CC therapy. The Ktomi1 nucleic acids may be used to diagnose, treat or
 CC monitor a disease caused by altered expression of human Ktomi1.
 CC Compositions comprising the nucleic acids, proteins or antibodies may be
 CC used to treat subjects having defects in Ktomi1 which can manifest as
 CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
 CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
 CC function. The sequence represents a probe used in the invention to
 CC scan the nt 1-1001 portion of human Ktomi1a (ABQ63322).
 XX
 SQ Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 other;

Query Match 63.3%; Score 11.4; DB 24; Length 17;
 Best Local Similarity 92.3%; Pred. No. 2.6e+04;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAGGGAGTCCAC 13
 |||||
 Db 17 CAGGGAGTCCCTC 5

RESULT 11
 ABQ63361/c
 ID ABQ63361 standard; DNA; 17 BP.
 XX
 AC ABQ63361;
 XX
 DT 20-AUG-2002 (first entry)
 XX
 DE Human Ktomi1a portion (ABQ63232) probe # 74.
 XX
 KW Human; Ktomi1a; Ktomi1; kidney tumour overexpressed membrane; cytostatic;
 KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
 KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
 OS Homo sapiens.
 XX
 PN WO200224750-A2.
 XX
 PD 28-MAR-2002.
 XX
 PF 21-SEP-2001; 2001WO-US29656.
 XX
 PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 PR 30-JAN-2001; 2001WO-US00661.
 PR 30-JAN-2001; 2001WO-US00662.
 PR 30-JAN-2001; 2001WO-US00663.
 PR 30-JAN-2001; 2001WO-US00664.
 PR 30-JAN-2001; 2001WO-US00665.
 PR 30-JAN-2001; 2001WO-US00666.
 PR 30-JAN-2001; 2001WO-US00667.
 PR 30-JAN-2001; 2001WO-US00668.
 PR 30-JAN-2001; 2001WO-US00669.
 PR 23-MAY-2001; 2001WO-US00670.
 PR 28-AUG-2001; 2001US-0864761.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Zhang J;
 XX
 DR WPI; 2002-479509/51.
 XX

PT New human kidney tumor overexpressed membrane (Ktomi1) protein and
 PT nucleic acids encoding the protein, useful for treating subjects having
 PT defects in Ktomi1 which can manifest as cancer of the kidney, or as a
 PT disorder of e.g., liver or bone
 XX
 PS Example 2; Page 167; 418pp; English.
 XX
 CC The invention relates to a novel isolated nucleic acid encoding human
 CC Ktomi1 (kidney tumour overexpressed membrane) protein. The protein of the
 CC invention has cytostatic activity. The nucleotide may have a use in gene
 CC therapy. The Ktomi1 nucleic acids may be used to diagnose, treat or
 CC monitor a disease caused by altered expression of human Ktomi1.
 CC Compositions comprising the nucleic acids, proteins or antibodies may be
 CC used to treat subjects having defects in Ktomi1 which can manifest as
 CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
 CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
 CC function. The sequence represents a probe used in the invention to
 CC scan the nt 1-1001 portion of human Ktomi1a (ABQ63232).
 XX
 SQ Sequence 17 BP; 3 A; 5 C; 5 G; 4 T; 0 other;

Query Match 63.3%; Score 11.4; DB 24; Length 17;
 Best Local Similarity 92.3%; Pred. No. 2.6e+04;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAGGGAGTCCAC 13
 |||||
 Db 16 CAGGGAGTCCCTC 4

RESULT 12
 ABQ63362/c
 ID ABQ63362 standard; DNA; 17 BP.
 XX
 AC ABQ63362;
 XX
 DT 20-AUG-2002 (first entry)
 XX
 DE Human Ktomi1a portion (ABQ63232) probe # 75.
 XX
 KW Human; Ktomi1a; Ktomi1; kidney tumour overexpressed membrane; cytostatic;
 KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
 KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
 OS Homo sapiens.
 XX
 PN WO200224750-A2.
 XX
 PD 28-MAR-2002.
 XX
 PF 21-SEP-2001; 2001WO-US29656.
 XX
 PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 PR 30-JAN-2001; 2001WO-US00661.
 PR 30-JAN-2001; 2001WO-US00662.
 PR 30-JAN-2001; 2001WO-US00663.
 PR 30-JAN-2001; 2001WO-US00664.
 PR 30-JAN-2001; 2001WO-US00665.
 PR 30-JAN-2001; 2001WO-US00666.
 PR 30-JAN-2001; 2001WO-US00667.
 PR 30-JAN-2001; 2001WO-US00668.
 PR 30-JAN-2001; 2001WO-US00669.
 PR 30-JAN-2001; 2001WO-US00670.
 PR 23-MAY-2001; 2001US-0864761.
 PR 28-AUG-2001; 2001US-315676P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Zhang J;
 XX
 DR WPI; 2002-479509/51.
 XX

XX New human kidney tumor overexpressed membrane (KTOM1) protein and
 PT nucleic acids encoding the protein, useful for treating subjects having
 PT defects in KTOM1 which can manifest as cancer of the kidney, or as a
 PT disorder of e.g., liver or bone
 XX Example 2; Page 167; 418pp; English.
 XX The invention relates to a novel isolated nucleic acid encoding human
 CC KTOM1 (kidney tumor overexpressed membrane) protein. The protein of the
 CC invention has cytostatic activity. The nucleotide may have a use in gene
 CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
 CC monitor a disease caused by altered expression of human KTOM1.
 CC Compositions comprising the nucleic acids, proteins or antibodies may be
 CC used to treat subjects having defects in KTOM1 which can manifest as
 CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
 CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
 CC function. The sequence represents a probe used in the invention to
 CC scan the nt 1-1001 portion of human KTOM1a (AB063232).
 XX Sequence 17 BP; 3 A; 5 C; 5 G; 4 T; 0 other;

Query Match 63.3%; Score 11.4; DB 24; Length 17;
 Best Local Similarity 92.3%; Pred. No. 2.6e+04;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGGGAGTCCAC 13
 Db 15 CAGGGAGTCCCTC 3

RESULT 13
 AB063363/c
 ID AB063363 standard; DNA; 17 BP.

XX AC AB063363;
 XX 20-AUG-2002 (first entry)
 XX Human KTOM1a portion (AB063232) probe # 76.

XX Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
 KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
 KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
 OS Homo sapiens.

XX WO200224750-A2.

XX 28-MAR-2002.

XX 21-SEP-2001; 2001WO-US29656.

XX 21-SEP-2000; 2000US-234687P.

XX 27-SEP-2000; 2000US-236359P.

XX 04-OCT-2000; 2000GB-0024263.

XX 30-JAN-2001; 2001WO-US00661.

XX 30-JAN-2001; 2001WO-US00662.

XX 30-JAN-2001; 2001WO-US00663.

XX 30-JAN-2001; 2001WO-US00664.

XX 30-JAN-2001; 2001WO-US00665.

XX 30-JAN-2001; 2001WO-US00666.

XX 30-JAN-2001; 2001WO-US00667.

XX 30-JAN-2001; 2001WO-US00669.

XX 23-MAY-2001; 2001WO-US00670.

XX 28-AUG-2001; 2001US-0864761.

XX 28-AUG-2001; 2001US-315676P.

XX (AEOM-) AEOMICA INC.

XX Zhang J;

XX PI

DR WPI; 2002-479509/51.

XX New human kidney tumor overexpressed membrane (KTOM1) protein and
 PT nucleic acids encoding the protein, useful for treating subjects having
 PT defects in KTOM1 which can manifest as cancer of the kidney, or as a
 PT disorder of e.g., liver or bone
 XX Example 2; Page 167; 418pp; English.

XX The invention relates to a novel isolated nucleic acid encoding human

CC KTOM1 (kidney tumor overexpressed membrane) protein. The protein of the
 CC invention has cytostatic activity. The nucleotide may have a use in gene
 CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
 CC monitor a disease caused by altered expression of human KTOM1.
 CC Compositions comprising the nucleic acids, proteins or antibodies may be
 CC used to treat subjects having defects in KTOM1 which can manifest as
 CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
 CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
 CC function. The sequence represents a probe used in the invention to
 CC scan the nt 1-1001 portion of human KTOM1a (AB063232).

XX Sequence 17 BP; 3 A; 4 C; 6 G; 4 T; 0 other;

Query Match 63.3%; Score 11.4; DB 24; Length 17;
 Best Local Similarity 92.3%; Pred. No. 2.6e+04;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGGGAGTCCAC 13
 Db 14 CAGGGAGTCCCTC 2

RESULT 14

AB063364/c

ID AB063364 standard; DNA; 17 BP.

XX AC AB063364;

XX 20-AUG-2002 (first entry)

XX Human KTOM1a portion (AB063232) probe # 77.

XX Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
 KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
 KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
 OS Homo sapiens.

XX WO200224750-A2.

XX 28-MAR-2002.

XX 21-SEP-2001; 2001WO-US29656.

XX 21-SEP-2000; 2000US-234687P.

XX 27-SEP-2000; 2000US-236359P.

XX 04-OCT-2000; 2000GB-0024263.

XX 30-JAN-2001; 2001WO-US00661.

XX 30-JAN-2001; 2001WO-US00662.

XX 30-JAN-2001; 2001WO-US00663.

XX 30-JAN-2001; 2001WO-US00664.

XX 30-JAN-2001; 2001WO-US00665.

XX 30-JAN-2001; 2001WO-US00666.

XX 30-JAN-2001; 2001WO-US00667.

XX 30-JAN-2001; 2001WO-US00668.

XX 30-JAN-2001; 2001WO-US00669.

XX 23-MAY-2001; 2001WO-US00670.

XX 28-AUG-2001; 2001US-0864761.

XX 28-AUG-2001; 2001US-315676P.

XX (AEOM-) AEOMICA INC.

XX Zhang J;

XX PI

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 12, 2003, 10:26:01 ; Search time 1624 Seconds
(without alignments)
179.507 Million cell updates/sec

Title: US-09-622-964-6

Perfect score: 18

Sequence: 1 caggaggtccaccagcc 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 5800

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_othr:*

26: em_gss_pro:*

27: em_gss_rod:*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	10.4	57.8	19	9	AI056541
C 2	9.2	51.1	20	17	AZ848532
C 3	9	50.0	20	13	BM392896
C 4	9	50.0	20	13	BM394288
5	8.8	48.9	19	17	AZ351194
6	8.8	48.9	19	17	AZ788326

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

C 7	8.8	48.9	20	13	BM399755
C 8	8.6	47.8	19	17	AZ651069
C 9	8.6	47.8	20	17	AZ331568
10	8.4	46.7	19	10	AW063940
C 11	8.4	46.7	19	17	AZ323681
C 12	8.4	46.7	19	17	AZ411255
C 13	8.4	46.7	19	17	AZ775541
C 14	8.4	46.7	20	17	AZ773525
C 15	8.2	45.6	16	9	AI248882
16	8.2	45.6	19	17	AZ477353
C 17	8.2	45.6	19	17	AZ990851
C 18	8.2	45.6	20	13	BM395053
C 19	8	44.4	19	9	AI252235
C 20	8	44.4	19	17	AZ314143
C 21	8	44.4	19	17	AZ646713
22	8	44.4	20	17	AQ074235
C 23	8	44.4	20	17	AZ309592
24	8	44.4	20	17	AZ436106
C 25	8	44.4	20	17	AZ445379
C 26	8	44.4	20	17	AZ823352
C 27	8	44.4	20	17	AZ862319
C 28	7.8	43.3	18	14	BQ790001
C 29	7.8	43.3	18	17	AQ026356
C 30	7.8	43.3	19	17	AZ486389
C 31	7.8	43.3	19	17	AZ656937
C 32	7.8	43.3	20	9	AU254255
C 33	7.8	43.3	20	14	D18243
34	7.8	43.3	20	17	AZ309156
35	7.8	43.3	20	17	AZ478502
36	7.8	43.3	20	17	AZ490187
37	7.8	43.3	20	17	AZ835099
C 38	7.6	42.2	19	9	AI049374
C 39	7.6	42.2	19	17	AZ837373
C 40	7.6	42.2	20	17	AZ468517
41	7.4	41.1	16	9	AI590540
C 42	7.4	41.1	19	9	AA909236
C 43	7.4	41.1	19	9	AA928040
C 44	7.4	41.1	19	9	AI641650
45	7.4	41.1	19	9	AI758301

ALIGNMENTS

RESULT 1

AI056541/c

LOCUS

DEFINITION

AI056541

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AI056541
cy98c11.x1 Soares fetal_liver_spleen linear EST 29-SEP-1998
clone IMAGE:1673876 3' similar to TR:014731 014731
MEMBRANE-ASSOCIATED KINASE. [1] ; mRNA sequence.
AI056541
EST.
AI056541.1 GI:3330407
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 19)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ccgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: ccgaps-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 702 Std Error: 0.00
Seq Primer: -40ml3 fwd. Et from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..19
/organism="Homo sapiens"

Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and 14
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gil4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance.

BASE COUNT 0 a 5 c 14 g 1 t
 ORIGIN

Query Match 51.1%; Score 9.2; DB 17; Length 20;
 Best Local Similarity 78.6%; Pred. No. 2e+06;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGGGAGTCCAC 14
 ||||| |||||
 Db 15 CAGGGGGCCCCC 2

RESULT 3
 BM392896/c
 LOCUS
 DEFINITION
 50071-2-3-A03.f.1 Chilcoat/Turkewitz cDNA (small fraction)
 Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION
 BM392896
 VERSION
 BM392896.1 GI:18192949
 KEYWORDS
 EST.
 SOURCE
 ORGANISM
 Tetrahymena thermophila.
 Tetrahymena thermophila.
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomata; Tetrahymenina; Tetrahymena.
 REFERENCE
 1 (bases 1 to 20)
 AUTHORS
 Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel
 J., and Klobutcher, L.
 TITLE
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 JOURNAL
 Unpublished (2002)
 COMMENT
 Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.

FEATURES
 Location/Qualifiers
 1..20
 /organism="Tetrahymena thermophila"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (small fraction)"
 /note="Vector: Bluescript2 SK+; Details on library
 preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT 3 a 7 c 7 g 3 t
 ORIGIN

Query Match 50.0%; Score 9; DB 13; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.5e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGAGTCCCA 12
 |||||
 Db 11 GGAGTCCCA 3

/db_xref="taxon:9606"
 /clone_image="1673876"
 /clone_lib="Soares_fetal_liver_spleen_infls_sl"
 /sex="male"
 /dev_stage="20 week-post conception fetus"
 /lab_host="pH10B (ampicillin resistant)"
 /note="Organ: Liver and Spleen; Vector: p7T3D (Pharmacia)
 with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
 This is a subtracted version of the original Soares fetal
 liver spleen INFLS library. 1st strand cDNA was primed
 with a Pac I - oligo(dT) primer [5',
 AACTGGAAGATTAATTAAAGATCTTTTTTTTTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Pac I and cloned into the Pac I
 and Eco RI sites of the modified p7T3 vector. Library
 went through one round of normalization. Library
 constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 1 a 5 c 10 g 3 t
 ORIGIN

Query Match 57.8%; Score 10.4; DB 9; Length 19;
 Best Local Similarity 91.7%; Pred. No. 5.6e+05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTCCACACG 18
 |||||
 Db 16 GCCCACACG 5

RESULT 2
 AZ848532/c
 LOCUS
 DEFINITION
 2M0149M01R Mouse 10kb plasmid UGCCIM library Mus musculus genomic
 clone UGCC2M0149M01 R, DNA sequence.

ACCESSION
 AZ848532
 VERSION
 AZ848532.1 GI:13031714
 KEYWORDS
 GSS.
 SOURCE
 house mouse.
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 REFERENCE
 1 (bases 1 to 20)
 AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.,
 and Wright, D., Weiss, R.
 TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL
 Unpublished (2000)
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0149 row: M column: 01
 Seq primer: CACACAGGAACACGATGACG
 Class: plasmid ends
 High quality sequence stop: 20.

FEATURES
 Location/Qualifiers
 1..20
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCC2M0149M01"
 /clone_lib="Mouse 10kb plasmid UGCCIM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson

RESULT 4
BM394288/c
LOCUS
DEFINITION
50072-2-3-A03.f.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
BM394288
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
GI:18194341
Tetrahymena thermophila.
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
AUTHORS
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J., and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
JOURNAL
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
source
1..20
Location/Qualifiers
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT 3 a 7 g 3 t
ORIGIN
Query Match 50.0%; Score 9; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GGAGTCCCA 12
Db 11 GGAGTCCCA 3
|||||||

RESULT 5
A2351194
LOCUS
DEFINITION
1M0089A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0089A08 F, DNA sequence.
A2351194
ACCESSION
VERSION
KEYWORDS
SOURCE
GSS.
GI:10430431
house mouse.
ORGANISM
house musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0089 row: A column: 08
Seq primer: CGTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source
1..19
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="UUGC1M0089A08"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 7 a 7 c 1 g 4 t
ORIGIN
Query Match 48.9%; Score 8.8; DB 17; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.1e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AGTCCACCCAGC 17
Db 4 AATCCACCAAC 15
|||||||

RESULT 6
A2788326
LOCUS
DEFINITION
2M0035P16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0035P16 F, DNA sequence.
A2788326
ACCESSION
VERSION
KEYWORDS
SOURCE
GSS.
GI:12928014
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA

```

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0035 row: P column: 16
Seq primer: CGTTGTAACACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0035P16"
/clone_lib="Mouse 10kb plasmid UUGC1m library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1147321141qb1AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      7 a      6 c      3 g      3 t
ORIGIN
Query Match      48.9%; Score 8.8; DB 17; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.1e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 AGTCCACACG 17
        | | | | | | | |
DB      1 ATTCCACCAAC 12

RESULT 7
BM399755/c
LOCUS      BM399755      20 bp mRNA linear EST 17-JAN-2002
DEFINITION      5009-0-60-H10.t.1 Chilcoat/Turkewitz cDNA (large fraction)
                Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION      BM399755
VERSION
KEYWORDS      EST.
SOURCE
ORGANISM      Tetrahymena thermophila.
                Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
                Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
AUTHORS      Turkewitz,A.P., Karter,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel
                J. and Klobutcher,L.
TITLE      EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL
COMMENT      Unpublished (2002)
                Contact: Turkewitz AP
                Molecular Genetics and Cell Biology
                University of Chicago
                920 E. 58th Street, Chicago, IL 60637, USA
                Tel: 773 702 4374
                Fax: 773 702 3172
                Email: apturkew@midway.uchicago.edu
                Seq primer: T3.

```

```

FEATURES
source
Location/Qualifiers
1. .20
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: BlueScript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT      1 a      6 c      10 g      3 t
ORIGIN
Query Match      48.9%; Score 8.8; DB 13; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.1e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 GGGAGTCCAC 14
        | | | | | | | |
DB      12 GGGAGTCCAC 1

RESULT 8
AZ651069/c
LOCUS      AZ651069      19 bp DNA linear GSS 14-DEC-2000
DEFINITION      1M0521L06R Mouse 10kb plasmid UUGC1m library Mus musculus genomic
                clone UUGC1M0521L06 R, DNA sequence.
ACCESSION      AZ651069
VERSION
KEYWORDS      GSS.
SOURCE
ORGANISM      Mus musculus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
                Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
                M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                and Wright,D., Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
                plasmid inserts
JOURNAL
COMMENT      Unpublished (2000)
                Contact: Robert B. Weiss
                University of Utah Genome Center
                University of Utah
                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                84112, USA
                Tel: 801 585 5606
                Fax: 801 585 7177
                Email: ddunn@genetics.utah.edu
                Insert Length: 10000 Std Error: 0.00
                Plate: 0521 row: L column: 06
                Seq primer: CACACAGGAACAGCATGACG
                Class: plasmid ends
                High quality sequence stop: 19.
FEATURES
source
Location/Qualifiers
1. .19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0521L06"
/clone_lib="Mouse 10kb plasmid UUGC1m library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to

```

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (gii4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT
ORIGIN

Query Match 47.8%; Score 8.6; DB 17; Length 19;
Best Local Similarity 73.3%; Pred. No. 3.8e+06;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GGAGTCCACACGAC 17
Db 15 GGGGGTCCCAAGAC 1

RESULT 9
A2331568
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

20 bp DNA linear GSS 29-SEP-2000
clone UUGCLM0059N03 R, DNA sequence.
A2331568
A2331568.1 GI:10394387
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20).
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0059 row: N column: 03

Seq primer: CACACAGGACACGATGACC

Class: plasmid ends

High quality sequence stop: 20.

FEATURES

Location/Qualifiers
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0059N03"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (gii4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT
ORIGIN

Query Match 46.7%; Score 8.4; DB 10; Length 19;
Best Local Similarity 90.0%; Pred. No. 4.7e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CCACACGAC 18
|||||||

BASE COUNT
ORIGIN

Query Match 47.8%; Score 8.6; DB 17; Length 20;
Best Local Similarity 73.3%; Pred. No. 3.9e+06;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GGAGTCCACACGAC 18
Db 2 GCAGTCCCACTAAC 16

RESULT 10
AW063940
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL
MEDLINE
COMMENT

19 bp mRNA linear EST 07-DEC-2000
DP0975 KRIBB Human DP Intrathymic T-cell cDNA library Homo sapiens
CDNA 3', mRNA sequence.
AW063940
AW063940.1 GI:8887877
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 19)
Goh, S.-H., Park, J.-H., Lee, Y.-J., Lee, H.-S., Lee, I.-C.,
Park, J.-H., Kim, Y.-S. and Lee, C.-C.
Gene expression profile and identification of differentially
expressed transcripts during human intrathymic T-cell development
by cDNA sequencing analysis
Genomics 70 (1), 1-18 (2000)
20541704
Contact: Sung-Ho Goh
Genome Center
Korea Research Institute of Bioscience and Biotechnology
Oun-dong 52, Yu Sung-Gu, Daejeon 305-333, Republic of Korea
Tel: 82-42-860-4473
Fax: 82-42-860-4479
Email: gohsh@mail.kribb.re.kr
Seq primer: T7
High quality sequence stop: 15
POLYA=No.

FEATURES
source

Location/Qualifiers
1..19
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="KRIBB Human DP Intrathymic T-cell cDNA
library"
/tissue_type="Thymus"
/cell_type="Intrathymic T-cell"
/dev_stage="CD3+4+8+ double positive stage"
/note="Vector: pGEM-T; cDNA was made from total
cytoplasmic RNA of sorted human intrathymic CD3+4+8+
T-cell, adaptor ligated, amplified with PCR, and cloned
into pGEM-T vector."
8 a 7 c 3 g 1 t

BASE COUNT
ORIGIN

Query Match 46.7%; Score 8.4; DB 10; Length 19;
Best Local Similarity 90.0%; Pred. No. 4.7e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CCACACGAC 18
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Db          1  CCCACGATC 10

RESULT 11
A2323681/c
LOCUS
DEFINITION 19 bp DNA linear GSS 29-SEP-2000
clone UUGCLM0045E13F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0045E13 F, DNA sequence.
ACCESSION  A2323681
VERSION     A2323681.1 GI:10378640
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 19)
REFERENCE
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL
COMMENT    Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0045 row: E column: 13
            Seq primer: CGTGTAAACGACGCGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
            Location/Qualifiers
                1. 19
                /organism="Mus musculus"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGCLM0045E13"
                /clone_lib="Mouse 10kb plasmid UUGCLM library"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pWD42 (gi14732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
BASE COUNT      2 a      5 c      8 g      4 t
ORIGIN
Query Match      46.7%; Score 8.4; DB 17; Length 19;
Best Local Similarity 90.0%; Pred. No. 4.7e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9  CCCACGATC 18
        ||||| |||

Db          18  CCCACGGCC 9

RESULT 12
A2411255/c
LOCUS
DEFINITION 19 bp DNA linear GSS 03-OCT-2000
clone UUGCLM0184C18 F, DNA sequence.
ACCESSION  A2411255
VERSION     A2411255.1 GI:10535268
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 19)
REFERENCE
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL
COMMENT    Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0184 row: C column: 18
            Seq primer: CGTGTAAACGACGCGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
            Location/Qualifiers
                1. 19
                /organism="Mus musculus"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGCLM0184C18"
                /clone_lib="Mouse 10kb plasmid UUGCLM library"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pWD42 (gi14732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
BASE COUNT      7 a      4 c      4 g      4 t
ORIGIN
Query Match      46.7%; Score 8.4; DB 17; Length 19;
Best Local Similarity 90.0%; Pred. No. 4.7e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6  AGTCCACCA 15
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```

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Db          10 ACTCACCA 1

RESULT 13
LOCUS    A2775541/c
DEFINITION 2M0008H17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0008H17 F, DNA sequence.
ACCESSION A2775541
VERSION   A2775541.1 GI:12902185
KEYWORDS  GSS,
SOURCE    house mouse.
ORGANISM  Mus musculus
REFERENCE
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0008 row: H column: 17
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES
Location/Qualifiers
1..19
/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="UUGC2M0008H17"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      0 a      2 c      14 g      3 t
ORIGIN
Query Match      46.7%; Score 8.4; DB 17; Length 19;
Best Local Similarity 66.7%; Pred. No. 4.7e+06;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1 CAGGAGTCCACGACC 18
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```

Db          18 CACAGAGCCCCCCCCC 1

RESULT 14
LOCUS    A2773525/c
DEFINITION 2M0001B04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0001B04 F, DNA sequence.
ACCESSION A2773525
VERSION   A2773525.1 GI:12897980
KEYWORDS  GSS,
SOURCE    house mouse.
ORGANISM  Mus musculus
REFERENCE
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0001 row: B column: 04
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES
Location/Qualifiers
1..20
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0001B04"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      2 a      4 c      7 g      7 t
ORIGIN
Query Match      46.7%; Score 8.4; DB 17; Length 20;
Best Local Similarity 90.0%; Pred. No. 4.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 TCCACGACC 17
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Db 15 TCACACCAGC 6

RESULT 15
AI248882 16 bp mRNA linear EST 10-NOV-1998
LOCUS qu73e07.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:1977732 3',
DEFINITION similar to SW:CAL3_BOVIN P04258 COLLAGEN ALPHA 1(III) CHAIN. ;,
mRNA sequence.

ACCESSION AI248882
VERSION AI248882.1 GI:3844279
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
REFERENCE National Cancer Institute / National Institute of Neurological
AUTHORS Disorders and Stroke, Brain Tumor Genome Anatomy Project
TITLE (CGAP/BTGA), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
unknown library type
Trace considered overall poor quality
Insert Length: 1913 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..16
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1977732"
/clone_lib="NCI_CGAP_Brn35"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site:1; SalI;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.33 kb. Tumor types include:
meningioma, oligodendroglioma, astrocytoma (grade II),
medulloblastoma, astrocytoma (grade IV). Life Technologies
catalog #: 11544-012"
BASE COUNT 2 a 10 c 4 g 0 t
ORIGIN

Query Match 45.6%; Score 8.2; DB 9; Length 16;
Best Local Similarity 76.9%; Pred. No. 5.7e+06;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 AGTCCACACGCC 18
||| ||||| |
Db 1 AGGCCCCACCCGCC 13.

Search completed: July 12, 2003, 11:44:57
Job time : 1631 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2003, 10:39:36 ; Search time 47 Seconds
(without alignments)
117.451 Million cell updates/sec

Title: US-09-622-964-6

Perfect score: 18

Sequence: 1 caggaggtccaccagcc 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 247290

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/1/lna/5A-COMB.seq:*
- 2: /cgn2_6/ptodata/1/lna/5B-COMB.seq:*
- 3: /cgn2_6/ptodata/1/lna/6A-COMB.seq:*
- 4: /cgn2_6/ptodata/1/lna/6B-COMB.seq:*
- 5: /cgn2_6/ptodata/1/lna/PCTUS-COMB.seq:*
- 6: /cgn2_6/ptodata/1/lna/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	12.4	68.9	20	4	US-09-294-531B-23
2	11.4	63.3	18	4	US-09-630-706-61
3	11.2	62.2	20	4	US-08-397-220B-64
4	11.2	62.2	20	4	US-08-650-093C-64
5	11.2	62.2	20	4	US-08-270-391-10
6	10.8	60.0	17	2	US-08-292-620A-1684
7	10.8	60.0	17	2	US-08-292-620A-1727
8	10.8	60.0	17	2	US-08-292-620A-1768
9	10.8	60.0	17	2	US-08-292-620A-1937
10	10.8	60.0	17	2	US-08-292-620A-1937
11	10.8	60.0	17	3	US-09-071-845-1684
12	10.8	60.0	17	3	US-09-071-845-1727
13	10.8	60.0	17	3	US-09-071-845-1768
14	10.8	60.0	17	3	US-09-071-845-1937
15	10.8	60.0	17	4	US-09-040-774-5
16	10.8	60.0	18	3	US-09-189-760-4
17	10.8	60.0	18	3	US-09-188-811-4
18	10.8	60.0	18	4	US-09-514-422-4
19	10.8	60.0	19	1	US-08-584-040-8293
20	10.8	60.0	19	1	US-08-399-986B-19
21	10.8	60.0	20	1	US-08-493-754A-19
22	10.8	60.0	20	1	US-07-841-652-26
23	10.8	60.0	20	1	US-08-446-530-2
24	10.8	60.0	20	1	US-08-446-530-2
25	10.8	60.0	20	2	US-09-097-562-2
26	10.8	58.9	18	2	US-09-097-562-4
27	10.6	58.9	18	3	US-08-691-814B-58
					Sequence 14, Appl

c 28	10.6	58.9	18	4	US-09-387-044B-21
29	10.6	58.9	19	1	US-08-460-853-11
30	10.6	58.9	19	4	US-09-312-748-10
31	10.6	58.9	20	1	US-08-782-047-17
32	10.6	58.9	20	3	US-09-280-799-194
33	10.6	58.9	20	3	US-08-924-870A-17
34	10.4	57.8	15	1	US-08-363-240A-107
35	10.4	57.8	15	1	US-08-363-240A-636
36	10.4	57.8	15	1	US-08-584-040-7977
37	10.4	57.8	17	4	US-08-671-947-13
38	10.4	57.8	18	1	US-08-671-947-14
39	10.4	57.8	18	1	US-08-250-858A-31
40	10.4	57.8	20	2	US-08-756-806A-31
41	10.4	57.8	20	3	US-09-143-214-31
42	10.4	57.8	20	3	US-09-000-136-17
43	10.4	57.8	20	4	US-09-593-589-82
44	10.4	57.8	20	4	US-09-506-073-33
45	10.4	57.8	20	4	US-09-506-073-33

ALIGNMENTS

RESULT 1

US-09-294-531B-23/C
; Sequence 23, Application US/09294531B
; Patent No. 6372889
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Farrar, Theresa M.
; APPLICANT: Mauer, Mark F.
; APPLICANT: Grossmann, Angelika
; TITLE OF INVENTION: SOLUBLE PROTEIN ZTMP0-1
; FILE REFERENCE: 97-67
; CURRENT APPLICATION NUMBER: US/09/294,531B
; PRIOR FILING DATE: 1999-04-19
; PRIOR APPLICATION NUMBER: 60/082,513
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide 16037
US-09-294-531B-23

Query Match 68.9%; Score 12.4; DB 4; Length 20;
Best Local Similarity 92.9%; Pred. No. 9.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GAGTCCCAACAGCC 18

Db 14 GAGTCCCAACAGCC 1

RESULT 2

US-09-630-706-61
; Sequence 61, Application US/09630706
; Patent No. 6277640
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HER-3 EXPRESSION
; FILE REFERENCE: RTS-0053
; CURRENT APPLICATION NUMBER: US/09/630,706
; CURRENT FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 94
; SEQ ID NO 61
; LENGTH: 18
; TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-630-706-61

Query Match 63.3%; Score 11.4; DB 4; Length 18;
Best Local Similarity 92.3%; Pred. No. 2.9e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTCCACGAGCC 18
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Db 2 AGTCCACGAGCC 14

RESULT 3

US-08-397-220B-64
Sequence 64, Application US/08397220B
Patent No. 6284458
GENERAL INFORMATION:
APPLICANT: Anderson et al.
TITLE OF INVENTION: Compositions And Methods For Treatment
Of Hepatitis C Virus-Associated Diseases

NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
ZIP: 08002

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,220B
FILING DATE: 09-Mar-1995
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/01293
FILING DATE: 10-Sep-93
APPLICATION NUMBER: JP 5-87195
FILING DATE: 14-Apr-93
APPLICATION NUMBER: 07/945,289
FILING DATE: 10-Sep-92

ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-08-397-220B-64

Query Match 62.2%; Score 11.2; DB 4; Length 20;
Best Local Similarity 81.2%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGGGAGTCCACGAG 16
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Db 5 CAGGCAGTACCACAG 20

RESULT 4

US-08-650-093C-64
Sequence 64, Application US/08650093C
Patent No. 6391542
GENERAL INFORMATION:
APPLICANT: Kevin P. Anderson et al.
TITLE OF INVENTION: Compositions And Methods For Treatment Of
Hepatitis C Virus-Associated Diseases

NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: LICATA & TYRRELL P.C.
STREET: 66 E. Main Street
CITY: Marlton
STATE: NJ
COUNTRY: USA
ZIP: 08053

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WORDPERFECT 6.1 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,093C
FILING DATE: 17-May-1996
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/452,841
FILING DATE: May 30, 1995
APPLICATION NUMBER: 08/397,220
FILING DATE: March 9, 1995
APPLICATION NUMBER: 07/945,289
FILING DATE: September 10, 1992

ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-08-650-093C-64

Query Match 62.2%; Score 11.2; DB 4; Length 20;
Best Local Similarity 81.2%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGGGAGTCCACGAG 16
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Db 5 CAGGCAGTACCACAG 20

RESULT 5

US-09-270-391-10/C
Sequence 10, Application US/09270391A
Patent No. 6410233
GENERAL INFORMATION:
APPLICANT: de Belle, Ian
APPLICANT: Adamson, Eileen

APPLICANT: Marcola, Dan
TITLE OF INVENTION: Isolation and Identification of Control Sequences and
Factors Modulating Transcription
FILE REFERENCE: PS-00101.P.1
CURRENT APPLICATION NUMBER: US/09/270,391A
CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-270-391-10

Query Match 62.2%; Score 11.2; DB 4; Length 20;
Best Local Similarity 81.2%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 3 GGGAGTCCACAGCC 18

|||||

Db 17 GGGGTCCCTCAGCC 2

RESULT 6

US-08-292-620A-1684

; Sequence 1684, Application US/08292620A

; Patent No. 5837542

; GENERAL INFORMATION:

; APPLICANT: Susan Grimm

; APPLICANT: Dan T. Stinchcomb

; APPLICANT: James McSwiggen

; APPLICANT: Sean Sullivan

; APPLICANT: Kenneth G. Draper

; TITLE OF INVENTION: RIBOZYME TREATMENT OF

; TITLE OF INVENTION: DISEASES OR CONDITIONS

; TITLE OF INVENTION: RELATED TO LEVELS OF

; TITLE OF INVENTION: INTRACELLULAR ADHESION

; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)

; NUMBER OF SEQUENCES: 2390

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/292,620A

; FILING DATE: August 17, 1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA: including application

; PRIOR APPLICATION DATA: described below:

; APPLICATION NUMBER: 08/008,895

; FILING DATE: January 19, 1993

; APPLICATION NUMBER: 07/989,849

; FILING DATE: December 7, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 208/149

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 1684:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-292-620A-1684

Query Match 60.0%; Score 10.8; DB 2; Length 17;

Best Local Similarity 78.6%; Pred. No. 5.8e+03;

Matches 11; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

QY 3 GGGAGTCCACAGCC 16

|||||

Db 1 GGGAGUAUACACAG 14

RESULT 7

US-08-292-620A-1727

; Sequence 1727, Application US/08292620A

; Patent No. 5837542

; GENERAL INFORMATION:

; APPLICANT: Susan Grimm

; APPLICANT: Dan T. Stinchcomb

; APPLICANT: James McSwiggen

; APPLICANT: Sean Sullivan

; APPLICANT: Kenneth G. Draper

; TITLE OF INVENTION: RIBOZYME TREATMENT OF

; TITLE OF INVENTION: DISEASES OR CONDITIONS

; TITLE OF INVENTION: RELATED TO LEVELS OF

; TITLE OF INVENTION: INTRACELLULAR ADHESION

; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)

; NUMBER OF SEQUENCES: 2390

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/292,620A

; FILING DATE: August 17, 1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA: including application

; PRIOR APPLICATION DATA: described below:

; APPLICATION NUMBER: 08/008,895

; FILING DATE: January 19, 1993

; APPLICATION NUMBER: 07/989,849

; FILING DATE: December 7, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 208/149

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 1727:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-292-620A-1727

Query Match 60.0%; Score 10.8; DB 2; Length 17;

Best Local Similarity 78.6%; Pred. No. 5.8e+03;

Matches 11; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

QY 3 GGGAGTCCACAGCC 16

|||||

Db 3 GGGAGUAUACACAG 16

RESULT 8

US-08-292-620A-1768
; Sequence 1768, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292.620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1768:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-292-620A-1768

Query Match 60.0%; Score 10.8; DB 2; Length 17;
Best Local Similarity 78.6%; Pred. No. 5.8e+03;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 3 GGGAGTCCACCAG 16
|||||: |||||
Db 1 GGGAGUAUACCAG 14

RESULT 9

US-08-292-620A-1937
; Sequence 1937, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb

; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292.620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1937:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-292-620A-1937

Query Match 60.0%; Score 10.8; DB 2; Length 17;
Best Local Similarity 78.6%; Pred. No. 5.8e+03;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 3 GGGAGTCCACCAG 16
|||||: |||||
Db 3 GGGAGUAUACCAG 16

RESULT 10

US-09-071-845-1684
; Sequence 1684, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION

;; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
;; NUMBER OF SEQUENCES: 2390
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; CITY: Suite 4700
;; STATE: Los Angeles
;; COUNTRY: California
;; ZIP: 90071-2066
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/071,845
;; FILING DATE:
;; CLASSIFICATION:
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/292,620
;; FILING DATE: August 17, 1994
;; APPLICATION NUMBER: 08/008,895
;; FILING DATE: January 19, 1993
;; APPLICATION NUMBER: 07/989,849
;; FILING DATE: December 7, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 208/149
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;;
;; INFORMATION FOR SEQ ID NO: 1684:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
;; US-09-071-845-1684

Query Match 60.0%; Score 10.8; DB 3; Length 17;
Best Local Similarity 78.6%; Pred. No. 5.8e+03;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGGAGTCCACCAG 16
Db 1 GGGAGUACACCAG 14

RESULT 11

US-09-071-845-1727
; Sequence 1727, Application US/09071845
; Patent No. 6132967

GENERAL INFORMATION:

;; APPLICANT: Susan Grimm
;; APPLICANT: Dan T. Stinchcomb
;; APPLICANT: James McSwigen
;; APPLICANT: Sean Sullivan
;; APPLICANT: Kenneth G. Draper
;; TITLE OF INVENTION: RIBOZYME TREATMENT OF
;; TITLE OF INVENTION: DISEASES OR CONDITIONS
;; TITLE OF INVENTION: RELATED TO LEVELS OF
;; TITLE OF INVENTION: INTRACELLULAR ADHESION
;; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
;; NUMBER OF SEQUENCES: 2390
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; CITY: Suite 4700
;; STATE: Los Angeles

;; STATE: California
;; COUNTRY: U.S.A.
;; ZIP: 90071-2066
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/071,845
;; FILING DATE:
;; CLASSIFICATION:
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/292,620
;; FILING DATE: August 17, 1994
;; APPLICATION NUMBER: 08/008,895
;; FILING DATE: January 19, 1993
;; APPLICATION NUMBER: 07/989,849
;; FILING DATE: December 7, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 208/149
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;;
;; INFORMATION FOR SEQ ID NO: 1727:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
;; US-09-071-845-1727

Query Match 60.0%; Score 10.8; DB 3; Length 17;
Best Local Similarity 78.6%; Pred. No. 5.8e+03;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGGAGTCCACCAG 16
Db 3 GGGAGUACACCAG 16

RESULT 12

US-09-071-845-1768
; Sequence 1768, Application US/09071845
; Patent No. 6132967

GENERAL INFORMATION:

;; APPLICANT: Susan Grimm
;; APPLICANT: Dan T. Stinchcomb
;; APPLICANT: James McSwigen
;; APPLICANT: Sean Sullivan
;; APPLICANT: Kenneth G. Draper
;; TITLE OF INVENTION: RIBOZYME TREATMENT OF
;; TITLE OF INVENTION: DISEASES OR CONDITIONS
;; TITLE OF INVENTION: RELATED TO LEVELS OF
;; TITLE OF INVENTION: INTRACELLULAR ADHESION
;; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
;; NUMBER OF SEQUENCES: 2390
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; CITY: Suite 4700
;; STATE: Los Angeles
;; COUNTRY: California
;; ZIP: 90071-2066
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible


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; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071.845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292.620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008.895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989.849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1768:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-845-1768

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Query Match          60.0%; Score 10.8; DB 3; Length 17;
Best Local Similarity 78.6%; Pred. No. 5.8e+03;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy 3 GGGAGTCCACCAG 16
    |||||: |||||
Db 1 GGGAGUAUCCAG 14

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RESULT 13
US-09-071-845-1937
; Sequence 1937, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; NUMBER OF SEQUENCES: MOLECULE-1 (I-CAM-1)
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071.845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US/08/292.620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008.895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989.849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1937:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-845-1937

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Query Match          60.0%; Score 10.8; DB 3; Length 17;
Best Local Similarity 78.6%; Pred. No. 5.8e+03;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy 3 GGGAGTCCACCAG 16
    |||||: |||||
Db 3 GGGAGUAUCCAG 16

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RESULT 14
US-09-040-774-5
; Sequence 5, Application US/09040774
; Patent No. 6207811
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Kestila, Marjo
; APPLICANT: Lenkkeri, Ulla
; APPLICANT: Mannikko, Minna
; TITLE OF INVENTION: Nephlin Gene and Protein
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 S. Wacker Drive, Suite 3200
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/040,774
; FILING DATE: 18 MAR 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Chao, Mark
; REGISTRATION NUMBER: 37,293
; REFERENCE/DOCKET NUMBER: 97,842
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)913-0001
; TELEFAX: (312)913-0002
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer intron 23"

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US-09-040-774-5

Query Match 60.0%; Score 10.8; DB 4; Length 17;
Best Local Similarity 85.7%; Pred. No. 5.8e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CAGGGAGTCCACC 14
| | | | | | | | | | | | | | | | | |
Db 3 CGGGAGAGCCACC 16

RESULT 15

US-09-189-760-4
; Sequence 4, Application US/09189760
; Patent No. 6031078
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran
; TITLE OF INVENTION: NOVEL MTBX PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE OF INVENTION: THEREFOR
; FILE REFERENCE: MNI-046CP2
; CURRENT APPLICATION NUMBER: US/09/189,760
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/163,116
; EARLIER FILING DATE: 1998-09-29
; EARLIER APPLICATION NUMBER: 60/089,467
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: (PENDING)
; EARLIER FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-189-760-4

Query Match 60.0%; Score 10.8; DB 3; Length 18;
Best Local Similarity 85.7%; Pred. No. 5.8e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 GAGTCCCACAGCC 18
| | | | | | | | | | | | | | | | | |
Db 5 GAGTCCCAGCC 18

Search completed: July 12, 2003, 11:45:54
Job time : 49 secs